



results of **BLAST**

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1056307209-022108-8672

Query=

(27 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

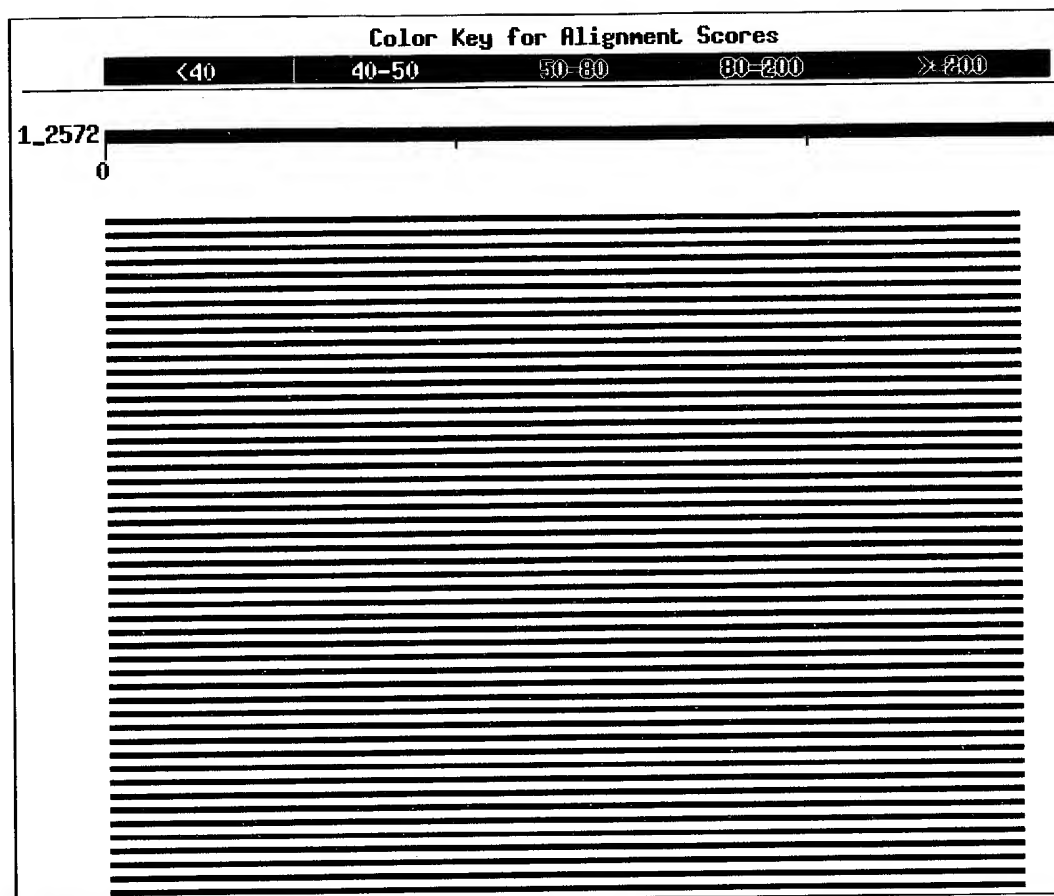
1,458,236 sequences; 468,339,122 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 96 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Related Structures

		Score	E	
Sequences producing significant alignments:		(bits)	Value	
gi 431446 gb AAA31468.1	surfactant protein A	61	4e-09	
gi 131413 sp P12842 PSPA_RABIT	Pulmonary surfactant-associa...	61	4e-09	
gi 382753 prf 1901176A	surfactant protein A	61	4e-09	
gi 1709872 sp P49874 PSPA_PIG	Pulmonary surfactant-associat...	60	7e-09	
gi 444733 prf 1908183A	surfactant-associated protein SP-A	60	8e-09	
gi 31543691 ref NP_075623.2	surfactant associated protein ...	60	8e-09	L
gi 464483 sp P35242 PSPA_MOUSE	Pulmonary surfactant-associa...	60	8e-09	L
gi 6601484 gb AAF18995.1 AF211856_1	pulmonary surfactant pr...	60	1e-08	
gi 8918631 dbj BAA97976.1	pulmonary surfactant protein A [...	60	1e-08	
gi 71967 pir LNHUPS	pulmonary surfactant protein A precurs...	59	1e-08	
gi 27501930 gb AAO13490.1	surfactant, pulmonary-associated...	59	1e-08	
gi 190672 gb AAA36520.1	pulmonary surfactant-associated pr...	59	1e-08	
gi 71969 pir LNHUP1	pulmonary surfactant protein A precurs...	59	1e-08	
gi 15788236 gb AAL07690.1 AF400580_1	pulmonary surfactant-a...	59	1e-08	
gi 27501922 gb AAO13486.1	surfactant, pulmonary-associated...	59	2e-08	
gi 13346504 ref NP_005402.2	surfactant, pulmonary-associat...	59	2e-08	L
gi 131412 sp P07714 PSPA_HUMAN	Pulmonary surfactant-associa...	59	2e-08	L
gi 1709873 sp P08427 PSPA_RAT	Pulmonary surfactant-associat...	59	2e-08	L
gi 206459 gb AAA41972.1	prepulmonary surfactant-associated...	59	2e-08	L
gi 1172693 sp P06908 PSPA_CANEA	Pulmonary surfactant-associ...	58	3e-08	

gi 71970 pir LNDGPS	pulmonary surfactant protein A precurs...	58	3e-08	
gi 8394337 ref NP_059025.1	pulmonary surfactant-associated...	58	4e-08	L
gi 57839 emb CAA31574.1	pulmonary surfactant protein A (AA...	58	4e-08	L
gi 13346506 ref NP_008857.1	surfactant, pulmonary-associat...	58	4e-08	L
gi 1709871 sp P50403 PSPA_CAVPO	Pulmonary surfactant-associ...	57	6e-08	
gi 6782434 gb AAF28384.1 AF133668_1	lung surfactant protein...	57	6e-08	
gi 20070752 gb AAH26229.1	Unknown (protein for MGC:22153) ...	56	2e-07	
gi 27805091 gb AAO22991.1	surfactant, pulmonary-associated...	48	4e-05	
gi 21361549 ref NP_003010.2	surfactant, pulmonary-associat...	48	4e-05	L
gi 464486 sp P35247 PSPD_HUMAN	Pulmonary surfactant-associa...	48	4e-05	L
gi 34767 emb CAA46152.1	lung surfactant protein D [Homo sa...	48	4e-05	L
gi 6573319 pdb 1B08 A	Chain A, Lung Surfactant Protein D (S...	47	1e-04	S
gi 6677921 ref NP_033186.1	surfactant associated protein D...	46	2e-04	L
gi 7949133 ref NP_037010.1	surfactant, pulmonary-associate...	46	2e-04	L
gi 27923966 sp P42916 CL43_BOVIN	Collectin-43 precursor (CL...	45	3e-04	L
gi 15420996 gb AAK97540.1 AF411083_1	surfactant protein A p...	45	4e-04	
gi 499385 emb CAA53511.1	collectin-43 [Bos taurus]	45	4e-04	L
gi 1083017 pir A53570	collectin-43 - bovine	45	5e-04	
gi 29570599 emb CAD69922.1	surfactant protein D [Bos taurus]	44	5e-04	L
gi 423283 pir S33603	surfactant protein D - bovine	44	5e-04	
gi 30794342 ref NP_851369.1	surfactant, pulmonary-associat...	44	5e-04	L
gi 21693526 gb AAM75337.1 AF512356_1	SFTPD [Macaca mulatta]	44	5e-04	
gi 6760482 gb AAF22145.2 AF132496_1	lung surfactant protein...	44	6e-04	
gi 395268 emb CAA50665.1	conglutinin [Bos taurus]	42	0.003	L
gi 461774 sp P23805 CONG_BOVIN	CONGLUTININ PRECURSOR >gi 34...	42	0.003	L
gi 31982388 ref NP_783630.2	conglutinin 1 [Bos taurus] >gi...	42	0.003	L
gi 27923754 sp Q8MHZ9 CL46_BOVIN	Collectin-46 precursor (CL...	40	0.008	L
gi 227513 prf 1705239A	mannan binding protein	37	0.068	
gi 5566370 gb AAD45377.1 AF164576_1	mannose-binding lectin ...	37	0.075	
gi 126677 sp P08661 MABC_RAT	Mannose-binding protein C prec...	37	0.078	L
gi 12083669 ref NP_073195.1	mannose-binding protein C (liv...	37	0.096	L
gi 1449044 gb AAB48071.1	mannose-binding protein C	37	0.12	
gi 6754656 ref NP_034906.1	mannose binding lectin, serum (...)	36	0.13	L
gi 233018 gb AAB19343.1	mannose-binding protein C; MBP-C [...]	36	0.13	L
gi 5453619 ref NP_006429.1	collectin sub-family member 10;...	36	0.18	L
gi 27806549 ref NP_776532.1	mannose-binding lectin (protei...	36	0.18	L
gi 27718903 ref XP_235331.1	similar to collectin sub-famil...	35	0.22	L
gi 27734138 ref NP_775598.1	collectin liver 1; collectin-L...	35	0.23	L
gi 27530341 dbj BAC53954.1	collectin-L1 [Mus musculus]	35	0.23	L
gi 14030460 gb AAK52907.1 AF360991_1	mannan-binding lectin ...	35	0.26	
gi 4557739 ref NP_000233.1	soluble mannose-binding lectin ...	35	0.26	L
gi 1449042 gb AAB48070.1	mannose-binding protein A	35	0.27	
gi 5911796 emb CAB56121.1	mannose-binding lectin [Homo sap...	35	0.28	
gi 5911794 emb CAB56045.1	mannose-binding lectin [Homo sap...	35	0.29	
gi 27718901 ref XP_235330.1	similar to collectin sub-famil...	35	0.31	L
gi 5911809 emb CAB56124.1	mannose-binding lectin [Homo sap...	35	0.33	
gi 22219167 pdb 1KZA 1	Chain 1, Complex Of Mbp-C And Man-A1...	35	0.34	S
gi 6729734 pdb 1BV4 A	Chain A, Apo-Mannose-Binding Protein...	35	0.38	S
gi 1421615 pdb 1RDI 1	Chain 1, Mannose-Binding Protein, Sub...	35	0.41	S

gi 1311344 pdb 1HUP	Alpha-Helical Coiled-Coil Mol_id: 1; ...	35	0.46	S
gi 4502253 ref NP_001172.1	asialoglycoprotein receptor 2 i...	33	0.86	L
gi 3318890 pdb 1BCJ 1	Chain 1, Mannose-Binding Protein-A Mu...	33	0.92	S
gi 3318887 pdb 1BCH 1	Chain 1, Mannose-Binding Protein-A Mu...	33	0.95	S
gi 3660143 pdb 1BUU A	Chain A, One Ho3+ Form Of Rat Mannose...	33	1.0	S
gi 18426877 ref NP_550436.1	asialoglycoprotein receptor 2 ...	33	1.1	L
gi 3420792 gb AAC31936.1	mannose-binding protein; MBP [Rat...	33	1.1	
gi 18426875 ref NP_550435.1	asialoglycoprotein receptor 2 ...	33	1.2	L
gi 22219120 pdb 1KX0 A	Chain A, Rat Mannose Protein A (H189...	33	1.2	S
gi 126675 sp P19999 MABA_RAT	Mannose-binding protein A prec...	33	1.2	
gi 1431805 pdb 1AFA 1	Chain 1, C-Type Lectin, Calcium-Bindi...	33	1.2	S
gi 6981188 ref NP_036731.1	mannose binding lectin 2, prote...	33	1.2	L
gi 13128972 ref NP_076932.1	hypothetical protein MGC3279 s...	33	1.2	L
gi 996129 pdb 1RTM 1	Chain 1, Mannose-Binding Protein A (Cl...	33	1.3	S
gi 22219117 pdb 1KWZ A	Chain A, Rat Mannose Protein A (H189...	33	1.4	S
gi 1942246 pdb 2KMB 1	Chain 1, Complex Of 3'-Neuac-Lewis-X ...	33	1.6	S
gi 230180 pdb 1MSB A	Chain A, Mannose Binding Protein A (Le...	33	1.8	S
gi 27717135 ref XP_234024.1	similar to hypothetical protei...	32	1.9	L
gi 10120821 pdb 1FIF A	Chain A, N-Acetylgalactosamine-Selec...	32	2.4	S
gi 12833584 dbj BAB22581.1	unnamed protein product [Mus mu...	32	3.5	L
gi 31455215 gb AAH09951.1	MGC3279 protein [Homo sapiens]	32	3.6	
gi 13898380 gb AAK48712.1 AF307972_1	E-selectin [Equus caba...	31	4.4	
gi 13898378 gb AAK48711.1 AF307971_1	E-selectin [Ovis aries]	31	5.2	
gi 6754654 ref NP_034905.1	mannose binding lectin, liver (...)	31	5.6	L
gi 28520762 ref XP_283054.1	RIKEN cDNA 1010001H16 [Mus mus...	30	8.7	L
gi 27806407 ref NP_776606.1	selectin E [endothelial adhesi...	30	9.0	L
gi 87597 pir A30359	P-selectin precursor - human	30	10.0	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|431446|gb|AAA31468.1| surfactant protein A
Length = 247

Score = 61.2 bits (147), Expect = 4e-09
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVMYTDGKWNDRNCLQSRLAICEF 27
EKCVMYTDGKWNDRNCLQ RL ICEF
Sbjct: 221 EKCVMYTDGKWNDRNCLQYRLVICEF 247

☐ >gi|131413|sp|P12842|PSPA_RABIT Pulmonary surfactant-associated protein A precursor (PSAP)
gi|71971|pir|LNRBPS pulmonary surfactant protein A precursor - rabbit
gi|165706|gb|AAA31465.1| apoprotein of surfactant
Length = 247

Score = 61.2 bits (147), Expect = 4e-09
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWDRNCLQSRLAICEF 27
EKCVELMYTDGKWDR+NCLQ RL ICEF
Sbjct: 221 EKCVELMYTDGKWDRNCLQYRLVICEF 247

☐ >gi|382753|prf||1901176A surfactant protein A
Length = 247

Score = 61.2 bits (147), Expect = 4e-09
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWDRNCLQSRLAICEF 27
EKCVELMYTDGKWDR+NCLQ RL ICEF
Sbjct: 221 EKCVELMYTDGKWDRNCLQYRLVICEF 247

☐ >gi|1709872|sp|P49874|PSPA_PIG Pulmonary surfactant-associated protein A precursor
(PSAP)
gi|762837|gb|AAA88403.1| pulmonary surfactant-associated protein A
Length = 249

Score = 60.5 bits (145), Expect = 7e-09
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWDRNCLQSRLAICEF 27
EKCVELMYTDG+WNDRNC Q RL AICEF
Sbjct: 223 EKCVELMYTDGQWDRNCCQYRLAICEF 249

☐ >gi|444733|prf||1908183A surfactant-associated protein SP-A
Length = 248

Score = 60.5 bits (145), Expect = 8e-09
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWDRNCLQSRLAICEF 27
EKCVELMYTDGKWDR+ CLQ RL AICEF
Sbjct: 222 EKCVELMYTDGKWDRNCLQYRLAICEF 248

☐ >gi|31543691|ref|NP_075623.2| ☒ surfactant associated protein A; surfactant pulmonary
protein A1 [Mus musculus]

gi|12835916|dbj|BAB23416.1| ☒ unnamed protein product [Mus musculus]
gi|12836233|dbj|BAB23565.1| ☒ unnamed protein product [Mus musculus]
gi|12847389|dbj|BAB27551.1| ☒ unnamed protein product [Mus musculus]
Length = 248

Score = 60.5 bits (145), Expect = 8e-09
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 EKCVELMYTDGKWNDR+ CLQ RLAICEF
 Sbjct: 222 EKCVELMYTDGKWNDRKGLQYRLAICEF 248

☐ >gi|464483|sp|P35242|PSPA_MOUSE ☒ Pulmonary surfactant-associated protein A precursor (PSAP)
 gi|477343|pir||A48853 pulmonary surfactant-associated protein SP-A - mouse
 gi|260453|gb|AAB24274.1| ☒ SP-A [Mus sp.]
 Length = 248

Score = 60.5 bits (145), Expect = 8e-09
 Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 EKCVELMYTDGKWNDR+ CLQ RLAICEF
 Sbjct: 222 EKCVELMYTDGKWNDRKGLQYRLAICEF 248

☐ >gi|6601484|gb|AAF18995.1|AF211856_1 pulmonary surfactant protein A [Ovis aries]
 gi|6901646|gb|AAF31148.1|AF076633_1 pulmonary surfactant-associated protein A [Ovis aries]
 Length = 248

Score = 59.7 bits (143), Expect = 1e-08
 Identities = 23/27 (85%), Positives = 26/27 (96%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 EKCVELMYTDGKWNDR+NCLQ RLAICEF
 Sbjct: 222 EKCVELMYTDGKWNDRKGLQYRLAICEF 248

☐ >gi|8918631|dbj|BAA97976.1| pulmonary surfactant protein A [Equus caballus]
 Length = 248

Score = 59.7 bits (143), Expect = 1e-08
 Identities = 24/27 (88%), Positives = 26/27 (96%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 EKCVELMYTDGKWNDR+CLQ RLAICEF
 Sbjct: 222 EKCVELMYTDGKWNDRSCLQYRLAICEF 248

☐ >gi|71967|pir||LNHUPS pulmonary surfactant protein A precursor (genomic clone) -
 gi|224709|prf||1111285A apoprotein, pulmonary surfactant
 Length = 248

Score = 59.3 bits (142), Expect = 1e-08
 Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 EKCVELMYTDGKWNDRNCL SRL ICEF
 Sbjct: 222 EKCVELMYTDGKWNDRNCLYSLRTICEF 248

☐ >gi|27501930|gb|AA013490.1| surfactant, pulmonary-associated protein A2 [Homo sa
Length = 248

Score = 59.3 bits (142), Expect = 1e-08
Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
E+CVEMYTDG+WNDNRNCL SRL ICEF
Sbjct: 222 EQCVEMYTDGQWNDNRNCLYSRLTICEF 248

☐ >gi|190672|gb|AAA36520.1| pulmonary surfactant-associated protein
Length = 248

Score = 59.3 bits (142), Expect = 1e-08
Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
E+CVEMYTDG+WNDNRNCL SRL ICEF
Sbjct: 222 EQCVEMYTDGQWNDNRNCLYSRLTICEF 248

☐ >gi|71969|pir||LNHUP1 pulmonary surfactant protein A precursor (clone 1A) - huma
Length = 248

Score = 59.3 bits (142), Expect = 1e-08
Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
E+CVEMYTDG+WNDNRNCL SRL ICEF
Sbjct: 222 EQCVEMYTDGQWNDNRNCLYSRLTICEF 248

☐ >gi|15788236|gb|AAL07690.1|AF400580.1 pulmonary surfactant-associated protein A
Length = 248

Score = 59.3 bits (142), Expect = 1e-08
Identities = 24/27 (88%), Positives = 26/27 (96%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
EKCVMYTDG+WNDR+CLQ RL AICEF
Sbjct: 222 EKCVMYTDGQWNDNRSLQYRLAICEF 248

☐ >gi|27501922|gb|AA013486.1| surfactant, pulmonary-associated protein A1 [Homo sa
Length = 248

Score = 59.3 bits (142), Expect = 2e-08
Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
E+CVEMYTDG+WNDNRNCL SRL ICEF

Sbjct: 222 EQCVEMYTDGQWNRNCLYSRLTICEF 248

☐ >gi|13346504|ref|NP_005402.2| **L** surfactant, pulmonary-associated protein A1; pulmonary surfactant-associated protein [Homo sapiens]
 gi|190565|gb|AAA36510.1| **L** pulmonary surfactant apoprotein precursor
 Length = 248

Score = 59.3 bits (142), Expect = 2e-08
 Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 E+CVEMYTDG+WNRNCL SRL ICEF
 Sbjct: 222 EQCVEMYTDGQWNRNCLYSRLTICEF 248

☐ >gi|131412|sp|P07714|PSPA_HUMAN **L** Pulmonary surfactant-associated protein A precursor (PSAP) (Alveolar proteinosis protein) (35 kDa pulmonary surfactant-associated protein)
 gi|71968|pir||LNHUP6 pulmonary surfactant protein A precursor (clone 6A) - human
 gi|190670|gb|AAA60211.1| **L** pulmonary surfactant-associated protein
 Length = 248

Score = 59.3 bits (142), Expect = 2e-08
 Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 E+CVEMYTDG+WNRNCL SRL ICEF
 Sbjct: 222 EQCVEMYTDGQWNRNCLYSRLTICEF 248

☐ >gi|1709873|sp|P08427|PSPA_RAT Pulmonary surfactant-associated protein A precursor (PSAP)
 gi|71972|pir||LNRTPS pulmonary surfactant protein A precursor - rat.
 gi|1147798|gb|AAA85516.1| **L** surfactant protein-A
 gi|1585793|prf||2202163A surfactant protein A
 Length = 248

Score = 58.9 bits (141), Expect = 2e-08
 Identities = 23/27 (85%), Positives = 24/27 (88%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
 EKCVELMYTDG WNR CLQ RLA+CEF
 Sbjct: 222 EKCVELMYTDGTWNRGCLQYRLAVCEF 248

☐ >gi|206459|gb|AAA41972.1| **L** prepulmonary surfactant-associated protein A
 Length = 257

Score = 58.9 bits (141), Expect = 2e-08
 Identities = 23/27 (85%), Positives = 24/27 (88%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 EKCVMYTDG WNDR CLQ RLA+CEF
 Sbjct: 231 EKCVMYTDGTWNRGCLQYRLAVCEF 257

☐ >gi|1172693|sp|P06908|PSPA_CANFA Pulmonary surfactant-associated protein A precursor (PSAP)
 gi|164052|gb|AAA30887.1| pulmonary surfactant apoprotein
 Length = 248

Score = 58.2 bits (139), Expect = 3e-08
 Identities = 22/27 (81%), Positives = 26/27 (96%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 E+CVEMYTDG+WN++NCLQ RLAICEF
 Sbjct: 222 EQCVMYTDGQWNNKNCLQYRLAICEF 248

☐ >gi|71970|pir||LNDGPS pulmonary surfactant protein A precursor - dog
 Length = 248

Score = 58.2 bits (139), Expect = 3e-08
 Identities = 22/27 (81%), Positives = 26/27 (96%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 E+CVEMYTDG+WN++NCLQ RLAICEF
 Sbjct: 222 EQCVMYTDGQWNNKNCLQYRLAICEF 248

☐ >gi|8394337|ref|NP_059025.1| ☒ pulmonary surfactant-associated glycoprotein A; Surfactant-associated protein 1 (pulmonary surfactant protein, SP-A); surfactant associated protein A [Rattus norvegicus]
 gi|57837|emb|CAA31573.1| ☒ pulmonary surfactant protein A (AA 1-248) [Rattus sp.]
 gi|206461|gb|AAA41973.1| ☒ pulmonary surfactant protein A (56 could be 29)
 Length = 248

Score = 58.2 bits (139), Expect = 4e-08
 Identities = 23/27 (85%), Positives = 24/27 (88%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 EKCVMYTDG WNDR CLQ RLA+CEF
 Sbjct: 222 EKCVMYTDGTWNRGCLQYRLAVCEF 248

☐ >gi|57839|emb|CAA31574.1| ☒ pulmonary surfactant protein A (AA 1-248) [Rattus sp.]
 Length = 248

Score = 58.2 bits (139), Expect = 4e-08
 Identities = 23/27 (85%), Positives = 24/27 (88%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 EKCVMYTDG WNDR CLQ RLA+CEF
 Sbjct: 222 EKCVMYTDGTWNRGCLQYRLAVCEF 248

☐ >gi|13346506|ref|NP_008857.1| ☒ surfactant, pulmonary-associated protein A2 [Homo sapiens]
gi|2119529|pir|I51921 pulmonary surfactant-associated protein A1 - human
gi|338049|gb|AAA60319.1| ☒ pulmonary surfactant-associated protein SP-A
Length = 248

Score = 58.2 bits (139), Expect = 4e-08
Identities = 22/27 (81%), Positives = 25/27 (92%)

Query: 1 EKCVE MYTDGKW NDRNCLQSRLAICEF 27
E+CV E MYTDG+W NDRNCL SRL IC+F
Sbjct: 222 EQCV E MYTDGQW NDRNCLYSRLTICDF 248

☐ >gi|1709871|sp|P50403|PSPA_CAVPO Pulmonary surfactant-associated protein A precursor (PSAP)
gi|1101817|gb|AAB82952.1| pulmonary surfactant protein A [Cavia porcellus]
Length = 247

Score = 57.4 bits (137), Expect = 6e-08
Identities = 22/27 (81%), Positives = 23/27 (85%)

Query: 1 EKCVE MYTDGKW NDRNCLQSRLAICEF 27
EKC E MY DG WND+NCLQSRL ICEF
Sbjct: 221 EKCA E MYLDGTW NDKNCLQSRLTICEF 247

☐ >gi|6782434|gb|AAF28384.1|AF133668.1 lung surfactant protein A [Sus scrofa]
Length = 116

Score = 57.4 bits (137), Expect = 6e-08
Identities = 24/27 (88%), Positives = 25/27 (92%)

Query: 1 EKCVE MYTDGKW NDRNCLQSRLAICEF 27
EKCVE MYTDG+W NDRNC Q RL AICEF
Sbjct: 90 EKCVE MYTDGQW NDRNCQQYRL AICEF 116

☐ >gi|20070752|gb|AAH26229.1| Unknown (protein for MGC:22153) [Homo sapiens]
Length = 117

Score = 55.8 bits (133), Expect = 2e-07
Identities = 23/27 (85%), Positives = 25/27 (92%)

Query: 1 EKCVE MYTDGKW NDRNCLQSRLAICEF 27
E+CV E MYTDG+W NDRNCL SRL ICEF
Sbjct: 91 EQCV E MYTDGQW NDRNCLYSRLTICEF 117

☐ >gi|27805091|gb|AAO22991.1| surfactant, pulmonary-associated protein D [Homo sapiens]
Length = 375

Score = 47.8 bits (112), Expect = 4e-05
Identities = 17/27 (62%), Positives = 22/27 (81%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++T+GKWNR C + RL +CEF
Sbjct: 349 EDCVEIFTNGKWNRACGEKRLVVCEF 375

☐ >gi|21361549|ref|NP_003010.2| **L** surfactant, pulmonary-associated protein D; surf
[Homo sapiens]
gi|18490171|gb|AAH22318.1| **L** Unknown (protein for MGC:22626) [Homo sapiens]
Length = 375

Score = 47.8 bits (112), Expect = 4e-05
Identities = 17/27 (62%), Positives = 22/27 (81%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++T+GKWNR C + RL +CEF
Sbjct: 349 EDCVEIFTNGKWNRACGEKRLVVCEF 375

☐ >gi|464486|sp|P35247|PSPD_HUMAN **L** Pulmonary surfactant-associated protein D prec
gi|346375|pir|A45225 pulmonary surfactant protein D precursor - human
gi|292507|gb|AAB59450.1| **L** surfactant protein D
Length = 375

Score = 47.8 bits (112), Expect = 4e-05
Identities = 17/27 (62%), Positives = 22/27 (81%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++T+GKWNR C + RL +CEF
Sbjct: 349 EDCVEIFTNGKWNRACGEKRLVVCEF 375

☐ >gi|34767|emb|CAA46152.1| **L** lung surfactant protein D [Homo sapiens]
Length = 375

Score = 47.8 bits (112), Expect = 4e-05
Identities = 17/27 (62%), Positives = 22/27 (81%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++T+GKWNR C + RL +CEF
Sbjct: 349 EDCVEIFTNGKWNRACGEKRLVVCEF 375

☐ >gi|6573319|pdb|1B08|A **S** Chain A, Lung Surfactant Protein D (Sp-D) (Fragment)
gi|6573320|pdb|1B08|B **S** Chain B, Lung Surfactant Protein D (Sp-D) (Fragment)
gi|6573321|pdb|1B08|C **S** Chain C, Lung Surfactant Protein D (Sp-D) (Fragment)
Length = 158

Score = 46.6 bits (109), Expect = 1e-04
Identities = 17/27 (62%), Positives = 22/27 (81%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 E CVE++T+GKWND C + RL +CEF
 Sbjct: 132 EDCVEIFTNGKWNDRACGEKRLVVCEF 158

☐ >gi|6677921|ref|NP_033186.1| ☒ surfactant associated protein D [Mus musculus]
 gi|1709879|sp|P50404|PSPD_MOUSE ☒ Pulmonary surfactant-associated protein D precu
 gi|1129062|gb|AAA92021.1| ☒ surfactant protein D
 gi|4877556|gb|AAD31380.1|AF047742.1 ☒ surfactant protein D precursor [Mus musculu
 gi|6524992|gb|AAF15277.1| ☒ surfactant protein-D [Mus musculus]
 gi|13277590|gb|AAH03705.1| ☒ Surfactant associated protein D [Mus musculus]
 Length = 374

Score = 45.8 bits (107), Expect = 2e-04
 Identities = 16/27 (59%), Positives = 22/27 (81%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 E CVE++T+G+WND+ C + RL ICEF
 Sbjct: 348 ENCVEIFTNGQWNDKACGEQRLVICEF 374

☐ >gi|7949133|ref|NP_037010.1| ☒ surfactant, pulmonary-associated protein D; Pulmo
 protein D [Rattus norvegicus]
 gi|464487|sp|P35248|PSPD_RAT PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR
 (CP4)
 gi|285429|pir||A42046 surfactant protein D - rat
 gi|207036|gb|AAA42170.1| ☒ primary translation product of SP-D
 Length = 374

Score = 45.8 bits (107), Expect = 2e-04
 Identities = 16/27 (59%), Positives = 22/27 (81%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 E CVE++T+G+WND+ C + RL ICEF
 Sbjct: 348 ENCVEIFTNGQWNDKACGEQRLVICEF 374

☐ >gi|27923966|sp|P42916|CL43_BOVIN Collectin-43 precursor (CL-43) (43 kDa collect
 gi|18252109|gb|AAL61855.1| ☒ 43kDa collectin precursor [Bos taurus]
 gi|18252111|gb|AAL61856.1| 43kDa collectin precursor [Bos taurus]
 Length = 321

Score = 45.1 bits (105), Expect = 3e-04
 Identities = 16/27 (59%), Positives = 20/27 (74%)

Query: 1 EKCVMYTDGKWNDNRNCLQSRLAICEF 27
 E C+E+Y+DG WND C + RL ICEF
 Sbjct: 295 ENCLEIYSDGNWNDIECREERLVICEF 321

☐ >gi|15420996|gb|AAK97540.1|AF411083.1 surfactant protein A precursor [Gallus ga
 Length = 222

Score = 44.7 bits (104), Expect = 4e-04
Identities = 18/27 (66%), Positives = 20/27 (74%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
EKCVELMYTDG W DR C RL +CE+
Sbjct: 196 EKCVELMYTDGNWKDRKCNLYRLTVCEY 222

☐ >gi|499385|emb|CAA53511.1| ☒ collectin-43 [Bos taurus]
Length = 301

Score = 44.7 bits (104), Expect = 4e-04
Identities = 16/27 (59%), Positives = 20/27 (74%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
E C+E+Y+DG WND C + RL ICEF
Sbjct: 275 ENCLEIYSDGNWWDIECREERLVICEF 301

☐ >gi|1083017|pir||A53570 collectin-43 - bovine
Length = 301

Score = 44.7 bits (104), Expect = 5e-04
Identities = 16/27 (59%), Positives = 20/27 (74%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
E C+E+Y+DG WND C + RL ICEF
Sbjct: 275 ENCLEIYSDGNWWDIECREERLVICEF 301

☐ >gi|29570599|emb|CAD69922.1| ☒ surfactant protein D [Bos taurus]
Length = 369

Score = 44.3 bits (103), Expect = 5e-04
Identities = 16/27 (59%), Positives = 21/27 (77%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
E CVE++ +GKWND+ C + RL ICEF
Sbjct: 343 ENCVEIFPNGKWNDKVCGEQRLVICEF 369

☐ >gi|423283|pir||S33603 surfactant protein D - bovine
Length = 369

Score = 44.3 bits (103), Expect = 5e-04
Identities = 16/27 (59%), Positives = 21/27 (77%)

Query: 1 EKCVELMYTDGKWNDRNCLQSRLAICEF 27
E CVE++ +GKWND+ C + RL ICEF
Sbjct: 343 ENCVEIFPNGKWNDKVCGEQRLVICEF 369

☐ >gi|30794342|ref|NP_851369.1| ☒ surfactant, pulmonary-associated protein D [Bos
gi|464485|sp|P35246|PSPD BOVIN PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSO
gi|415939|emb|CAA53510.1| ☒ lung surfactant protein D [Bos taurus]
Length = 369

Score = 44.3 bits (103), Expect = 5e-04
Identities = 16/27 (59%), Positives = 21/27 (77%)

Query: 1 EKCVELMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++ +GKWND+ C + RL ICEF
Sbjct: 343 ENCVEIFPNGKWNDKVCGEQRLVICEF 369

☐ >gi|21693526|gb|AAM75337.1|AF512356_1 SFTPD [Macaca mulatta]
Length = 88

Score = 44.3 bits (103), Expect = 5e-04
Identities = 17/27 (62%), Positives = 22/27 (81%)

Query: 1 EKCVELMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++T+GKWNDR C + RL +CEF
Sbjct: 62 EDCVEIFTNGKWNDRACGEKRLVVCEF 88

☐ >gi|6760482|gb|AAF22145.2|AF132496_1 lung surfactant protein D precursor; SPD; S
Length = 378

Score = 43.9 bits (102), Expect = 6e-04
Identities = 16/27 (59%), Positives = 21/27 (77%)

Query: 1 EKCVELMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++ +GKWND+ C + RL ICEF
Sbjct: 352 ENCVEIFPNGKWNDKACGELRLVICEF 378

☐ >gi|395268|emb|CAA50665.1| ☒ conglutinin [Bos taurus]
Length = 371

Score = 42.0 bits (97), Expect = 0.003
Identities = 16/27 (59%), Positives = 19/27 (70%)

Query: 1 EKCVELMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++ DGKWND C + L ICEF
Sbjct: 345 ENCVEIFPDGKWNDVPCSKQLLVICEF 371

☐ >gi|461774|sp|P23805|CONG_BOVIN CONGLUTININ PRECURSOR
gi|346501|pir|JN0450 conglutinin precursor - bovine
gi|285644|dbj|BAA03170.1| ☒ conglutinin [Bos taurus]
gi|514256|gb|AAB60624.1| ☒ conglutinin precursor [Bos taurus]
gi|22852250|dbj|BAA04983.2| ☒ conglutinin precursor [Bos taurus]
Length = 371

Score = 42.0 bits (97), Expect = 0.003
Identities = 16/27 (59%), Positives = 19/27 (70%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++ DGKWND C + L ICEF
Sbjct: 345 ENCVEIFPDGKWNDVPCSKQLLVICEF 371

☐ >gi|31982388|ref|NP_783630.2| ☒ L conglutinin 1 [Bos taurus]
gi|7441637|pir||I45878 conglutinin - bovine
gi|495013|gb|AAA20126.1| ☒ L conglutinin
Length = 371

Score = 42.0 bits (97), Expect = 0.003
Identities = 16/27 (59%), Positives = 19/27 (70%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE++ DGKWND C + L ICEF
Sbjct: 345 ENCVEIFPDGKWNDVPCSKQLLVICEF 371

☐ >gi|27923754|sp|Q8MHZ9|CL46_BOVIN Collectin-46 precursor (CL-46) (46 kDa collect
gi|21105685|gb|AAM34742.1|AF509589_1 ☒ L 46-kDa collectin precursor [Bos taurus]
gi|21105687|gb|AAM34743.1|AF509590_1 ☒ L 46-kDa collectin precursor [Bos taurus]
Length = 371

Score = 40.4 bits (93), Expect = 0.008
Identities = 15/27 (55%), Positives = 19/27 (70%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CV++Y +GKWND C + L ICEF
Sbjct: 345 ENCVQIYREGKWNDVPCSEPLLVICEF 371

☐ >gi|227513|prf||1705239A mannan binding protein
Length = 244

Score = 37.4 bits (85), Expect = 0.068
Identities = 15/27 (55%), Positives = 18/27 (66%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CV + T+GKWND C S L +CEF
Sbjct: 216 ENCVVLLTNGKWNDVPCSDSFLVVCEF 242

☐ >gi|5566370|gb|AAD45377.1|AF164576_1 mannose-binding lectin [Sus scrofa]
Length = 240

Score = 37.0 bits (84), Expect = 0.075
Identities = 15/27 (55%), Positives = 17/27 (62%)

Query: 1 EKCVEMYTDGKWNDNRNCLQSRLAICEF 27
E CVE+ DGKWND C A+CEF

Sbjct: 212 EHCVEILKDGGKWNDFCSSLAVCEF 238

☐ >gi|126677|sp|P08661|MABC_RAT Mannose-binding protein C precursor (MBP-C) (Mannose-binding protein) (RA-reactive factor P28A subunit) (RARF/P28A)
 gi|71974|pir|LNRTMC mannose-binding lectin C precursor - rat
 gi|56635|emb|CAA28687.1| ☒ MBP precursor (AA -18 to 226) [Rattus norvegicus]
 gi|357355|prf|1302194A mannan binding protein
 Length = 244

Score = 37.0 bits (84), Expect = 0.078
 Identities = 15/27 (55%), Positives = 18/27 (66%)

Query: 1 EKCVEYTDGKWNDRNCLQSRLAICEF 27
 E CV + T+GKWND C S L +CEF
 Sbjct: 216 ENCVELLTNGKWNDRVPCSDSFLVVEF 242

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Jun 22, 2003 2:33 AM
 Number of letters in database: 468,339,122
 Number of sequences in database: 1,458,236

Lambda	K	H
0.324	0.137	0.477

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 26,188,383
 Number of Sequences: 1458236
 Number of extensions: 349394
 Number of successful extensions: 1109
 Number of sequences better than 10.0: 100
 Number of HSP's better than 10.0 without gapping: 97
 Number of HSP's successfully gapped in prelim test: 26
 Number of HSP's that attempted gapping in prelim test: 1012
 Number of HSP's gapped (non-prelim): 123
 length of query: 27
 length of database: 468,339,122
 effective HSP length: 3
 effective length of query: 24
 effective length of database: 463,964,414
 effective search space: 11135145936
 effective search space used: 11135145936
 T: 11
 A: 40

X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 67 (30.4 bits)